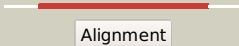



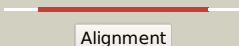

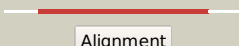

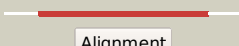

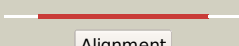

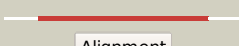




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2626c (-)_2952572_2953003
Date	Wed Aug 7 12:50:27 BST 2019
Unique Job ID	1f13d725c496fd56

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1y5ha3	 Alignment		99.9	96	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
2	c2qh1B_	 Alignment		99.9	23	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ta0289; PDBTitle: structure of ta289, a cbs-rubredoxin-like protein, in its fe+2-bound2 state
3	d1pvma4	 Alignment		99.9	23	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
4	c5nmuC_	 Alignment		99.9	25	PDB header: photosynthesis Chain: C: PDB Molecule: cbs-cp12; PDBTitle: structure of hexameric cbs-cp12 protein from bloom-forming2 cyanobacteria
5	d3ddja1	 Alignment		99.9	15	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
6	d2d4za3	 Alignment		99.9	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
7	c4fryA_	 Alignment		99.9	24	PDB header: signaling protein Chain: A: PDB Molecule: putative signal-transduction protein with cbs domains; PDBTitle: the structure of a putative signal-transduction protein with cbs2 domains from burkholderia ambifaria mc40-6
8	c2d4zB_	 Alignment		99.9	20	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein; PDBTitle: crystal structure of the cytoplasmic domain of the chloride channel2 clc-0
9	d2yzia1	 Alignment		99.9	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
10	d2o16a3	 Alignment		99.9	23	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
11	c6h1wA_	 Alignment		99.9	18	PDB header: unknown function Chain: A: PDB Molecule: mj1004; PDBTitle: crystal structure of protein mj1004 from mathanocaldococcus jannaschii

12	d2rc3a1	Alignment		99.9	25	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
13	c6cozB	Alignment		99.9	13	PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, c-terminal cytosolic domain
14	c4o9kB	Alignment		99.9	21	PDB header: isomerase Chain: B: PDB Molecule: arabinose 5-phosphate isomerase; PDBTitle: crystal structure of the cbs pair of a putative d-arabinose 5-2 phosphate isomerase from methylococcus capsulatus in complex with3 cmp-kdo
15	c4l3vB	Alignment		99.9	15	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: crystal structure of delta516-525 human cystathionine beta-synthase
16	c2pfiA	Alignment		99.9	15	PDB header: transport protein Chain: A: PDB Molecule: chloride channel protein clc-ka; PDBTitle: crystal structure of the cytoplasmic domain of the human2 chloride channel clc-ka
17	c4nocA	Alignment		99.9	12	PDB header: signaling protein Chain: A: PDB Molecule: putative signal transduction protein with cbs domains; PDBTitle: the crystal structure of a cbs domain-containing protein of unknown2 function from kribbella flavida dsm 17836.
18	c5aweA	Alignment		99.9	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative acetoin utilization protein, acetoin PDBTitle: crystal structure of a hypothetical protein, ttha0829 from thermus2 thermophilus hb8, composed of cystathionine-beta-synthase (cbs) and3 aspartate-kinase chorismate-mutase tyra (act) domains
19	d2yzqa1	Alignment		99.9	19	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
20	c5tr1A	Alignment		99.9	16	PDB header: transport protein Chain: A: PDB Molecule: chloride channel protein; PDBTitle: cryo-electron microscopy structure of a bovine clc-k chloride channel,2 alternate (class 2) conformation
21	d2j9la1	Alignment	not modelled	99.9	21	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
22	c5ks7A	Alignment	not modelled	99.9	21	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: carnitine transport atp-binding protein opuca; PDBTitle: crystal structure of listeria monocytogenes opuca cbs domain dimer in2 complex with cyclic-di-amp
23	c2ouxB	Alignment	not modelled	99.9	19	PDB header: transport protein Chain: B: PDB Molecule: magnesium transporter; PDBTitle: crystal structure of the soluble part of a magnesium transporter
24	d1vr9a3	Alignment	not modelled	99.9	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
25	c3fwrB	Alignment	not modelled	99.9	19	PDB header: transcription Chain: B: PDB Molecule: yqzb protein; PDBTitle: crystal structure of the cbs domains from the bacillus subtilis ccpn2 repressor complexed with adp
26	c6qvcB	Alignment	not modelled	99.9	13	PDB header: membrane protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: cryoem structure of the human clc-1 chloride channel, cbs state 1
27	c4esyB	Alignment	not modelled	99.9	29	PDB header: membrane protein Chain: B: PDB Molecule: cbs domain containing membrane protein; PDBTitle: crystal structure of the cbs domain of cbs domain containing membrane2 protein from sphaerobacter thermophilus
28	c1vr9B	Alignment	not modelled	99.9	20	PDB header: unknown function Chain: B: PDB Molecule: cbs domain protein/act domain protein; PDBTitle: crystal structure of a cbs domain pair/act domain protein (tm0892)2 from thermotoga maritima at 1.70 a resolution

29	c2yvxD_	Alignment	not modelled	99.9	27	PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte
30	c3fhmD_	Alignment	not modelled	99.9	25	PDB header: structural genomics, unknown function, n Chain: D: PDB Molecule: uncharacterized protein atu1752; PDBTitle: crystal structure of the cbs-domain containing protein atu1752 from2 agrobacterium tumefaciens
31	d2ouxax2	Alignment	not modelled	99.9	20	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
32	c3kpbA_	Alignment	not modelled	99.9	26	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein mj0100; PDBTitle: crystal structure of the cbs domain pair of protein mj01002 in complex with 5 -methylthioadenosine and s-adenosyl-l-3 methionine.
33	d1pbja3	Alignment	not modelled	99.9	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
34	c3lhhA_	Alignment	not modelled	99.9	17	PDB header: membrane protein Chain: A: PDB Molecule: cbs domain protein; PDBTitle: the crystal structure of cbs domain protein from shewanella2 oneidensis mr-1.
35	c3jtfB_	Alignment	not modelled	99.9	19	PDB header: transport protein Chain: B: PDB Molecule: magnesium and cobalt efflux protein; PDBTitle: the cbs domain pair structure of a magnesium and cobalt efflux protein2 from bordetella parapertussis in complex with amp
36	d2ooxe1	Alignment	not modelled	99.9	16	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
37	c3gbyA_	Alignment	not modelled	99.9	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ct1051; PDBTitle: crystal structure of a protein with unknown function ct10512 from chlorobium tepidum
38	c3fnaA_	Alignment	not modelled	99.9	20	PDB header: isomerase Chain: A: PDB Molecule: possible arabinose 5-phosphate isomerase; PDBTitle: crystal structure of the cbs pair of possible d-arabinose 5-phosphate2 isomerase yrbh from escherichia coli cft073
39	c3sl7B_	Alignment	not modelled	99.9	21	PDB header: membrane protein Chain: B: PDB Molecule: cbs domain-containing protein cbsx2; PDBTitle: crystal structure of cbs-pair protein, cbsx2 from arabidopsis thaliana
40	d2ef7a1	Alignment	not modelled	99.9	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
41	c3lfrB_	Alignment	not modelled	99.9	18	PDB header: transport protein Chain: B: PDB Molecule: putative metal ion transporter; PDBTitle: the crystal structure of a cbs domain from a putative metal ion2 transporter bound to amp from pseudomonas syringae to 1.55a
42	d2v8qe2	Alignment	not modelled	99.9	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
43	c1zfiA_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
44	c3pc3A_	Alignment	not modelled	99.9	13	PDB header: lyase Chain: A: PDB Molecule: cg1753, isoform a; PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
45	d2riha1	Alignment	not modelled	99.9	15	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
46	c3hf7A_	Alignment	not modelled	99.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized cbs-domain protein; PDBTitle: the crystal structure of a cbs-domain pair with bound amp from2 klebsiella pneumoniae to 2.75a
47	c2qlvF_	Alignment	not modelled	99.9	18	PDB header: transferase/protein binding Chain: F: PDB Molecule: nuclear protein snf4; PDBTitle: crystal structure of the heterotrimer core of the s. cerevisiae ampk2 homolog snf1
48	c4gqvA_	Alignment	not modelled	99.9	26	PDB header: protein binding Chain: A: PDB Molecule: cbs domain-containing protein cbsx1, chloroplastic; PDBTitle: crystal structure of cbs-pair protein, cbsx1 from arabidopsis thaliana
49	c3ocmA_	Alignment	not modelled	99.9	17	PDB header: membrane protein Chain: A: PDB Molecule: putative membrane protein; PDBTitle: the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
50	c3nqrD_	Alignment	not modelled	99.9	19	PDB header: transport protein Chain: D: PDB Molecule: magnesium and cobalt efflux protein corc; PDBTitle: a putative cbs domain-containing protein from salmonella typhimurium2 lt2
51	c2emqA_	Alignment	not modelled	99.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: hypothetical conserved protein (gk1048) from geobacillus kaustophilus
52	c2p9mD_	Alignment	not modelled	99.9	24	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein mj0922; PDBTitle: crystal structure of conserved hypothetical protein mj0922 from2 methanocaldococcus jannaschii dsm 2661
53	c3kxrA_	Alignment	not modelled	99.9	19	PDB header: transport protein Chain: A: PDB Molecule: magnesium transporter, putative; PDBTitle: structure of the cystathionine beta-synthase pair domain of the2 putative mg2+ transporter so5017 from shewanella oneidensis mr-1.

54	c3i8nB_	Alignment	not modelled	99.9	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein vp2912; PDBTitle: a domain of a conserved functionally known protein from2 vibrio parahaemolyticus rimd 2210633.
55	d1o50a3	Alignment	not modelled	99.9	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
56	c3lv9A_	Alignment	not modelled	99.8	19	PDB header: membrane protein Chain: A: PDB Molecule: putative transporter; PDBTitle: crystal structure of cbs domain of a putative transporter from2 clostridium difficile 630
57	c2v8qE_	Alignment	not modelled	99.8	18	PDB header: transferase Chain: E: PDB Molecule: 5'-amp-activated protein kinase subunit gamma-1; PDBTitle: crystal structure of the regulatory fragment of mammalian2 ampk in complexes with amp
58	c5g5rA_	Alignment	not modelled	99.8	22	PDB header: hydrolase Chain: A: PDB Molecule: site-2 protease; PDBTitle: cbs domain tandem of site-2 protease from archaeoglobus fulgidus in2 complex with llama nanobody - apo form
59	c2qr1E_	Alignment	not modelled	99.8	18	PDB header: transferase Chain: E: PDB Molecule: protein c1556.08c; PDBTitle: crystal structure of the adenylate sensor from amp-activated protein2 kinase in complex with adp
60	d2yvxa2	Alignment	not modelled	99.8	27	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
61	c5ohxB_	Alignment	not modelled	99.8	14	PDB header: lyase Chain: B: PDB Molecule: cystathionine beta-synthase; PDBTitle: structure of active cystathionine b-synthase from apis mellifera
62	d1yava3	Alignment	not modelled	99.8	23	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
63	d2nyca1	Alignment	not modelled	99.8	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
64	c4z87B_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
65	d2ooxe2	Alignment	not modelled	99.8	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
66	c3lqnA_	Alignment	not modelled	99.8	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cbs domain protein; PDBTitle: crystal structure of cbs domain-containing protein of2 unknown function from bacillus anthracis str. ames ancestor
67	c4hg0A_	Alignment	not modelled	99.8	18	PDB header: transport protein Chain: A: PDB Molecule: magnesium and cobalt efflux protein corc; PDBTitle: crystal structure of magnesium and cobalt efflux protein corc,2 northeast structural genomics consortium (nesg) target er40
68	c2yvzA_	Alignment	not modelled	99.8	25	PDB header: transport protein Chain: A: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte cytosolic domain,2 mg2+-free form
69	d2v8qe1	Alignment	not modelled	99.8	17	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
70	c1yavB_	Alignment	not modelled	99.8	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein bsu14130; PDBTitle: crystal structure of cbs domain-containing protein yukl2 from bacillus subtilis
71	d3ddja2	Alignment	not modelled	99.8	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
72	c3ocmB_	Alignment	not modelled	99.8	16	PDB header: membrane protein Chain: B: PDB Molecule: putative membrane protein; PDBTitle: the crystal structure of a domain from a possible membrane protein of2 bordetella parapertussis
73	c3orgB_	Alignment	not modelled	99.8	18	PDB header: transport protein Chain: B: PDB Molecule: cmclc; PDBTitle: crystal structure of a eukaryotic clc transporter
74	c3tsdA_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp
75	c3ocoB_	Alignment	not modelled	99.8	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hemolysin-like protein containing cbs domains; PDBTitle: the crystal structure of a hemolysin-like protein containing cbs2 domain of oenococcus oeni psu
76	c4iy3B_	Alignment	not modelled	99.8	15	PDB header: metal transport Chain: B: PDB Molecule: metal transporter cnm4; PDBTitle: structural and ligand binding properties of the bateman domain of2 human magnesium transporters cnm2 and cnm4
77	d1zfja4	Alignment	not modelled	99.8	14	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
78	c3ctuB_	Alignment	not modelled	99.8	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: cbs domain protein; PDBTitle: crystal structure of cbs domain protein from streptococcus2 pneumoniae tigr4 PDB header: hydrolase

79	c3l31B_	Alignment	not modelled	99.8	28	Chain: B: PDB Molecule: probable manganase-dependent inorganic PDBTitle: crystal structure of the cbs and drtg domains of the2 regulatory region of clostridium perfringens3 pyrophosphatase complexed with the inhibitor, amp
80	c5x8oA_	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
81	c5lipA_	Alignment	not modelled	99.8	22	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/carnitine/choline abc transporter%2c atp- PDBTitle: staphylococcus aureus opuca
82	c3ddjA_	Alignment	not modelled	99.8	15	PDB header: amp-binding protein Chain: A: PDB Molecule: rcbs domain-containing protein; PDBTitle: crystal structure of a cbs domain-containing protein in complex with2 amp (sso3205) from sulfolobus solfataricus at 1.80 a resolution
83	c3kh5A_	Alignment	not modelled	99.8	23	PDB header: unknown function Chain: A: PDB Molecule: protein mj1225; PDBTitle: crystal structure of protein mj1225 from methanocaldococcus2 jannaschii, a putative archaeal homolog of g-ampk.
84	c2yzqA_	Alignment	not modelled	99.8	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ph1780; PDBTitle: crystal structure of uncharacterized conserved protein from2 pyrococcus horikoshii
85	c4qfsC_	Alignment	not modelled	99.8	16	PDB header: signaling protein/inhibitor/activator Chain: C: PDB Molecule: 5'-amp-activated protein kinase subunit gamma-1; PDBTitle: structure of ampk in complex with br2-a769662core activator and2 staurosporine inhibitor
86	c3oi8B_	Alignment	not modelled	99.8	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of functionally unknown conserved protein domain2 from neisseria meningitidis mc58
87	d2yzqa2	Alignment	not modelled	99.7	25	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
88	c4dqwB_	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
89	c4fxsA_	Alignment	not modelled	99.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid
90	d1jcna4	Alignment	not modelled	99.0	18	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
91	c3fioB_	Alignment	not modelled	99.0	21	PDB header: nucleotide binding protein, metal bindin Chain: B: PDB Molecule: a cystathionine beta-synthase domain protein PDBTitle: crystal structure of a fragment of a cystathionine beta-2 synthase domain protein fused to a zn-ribbon-like domain
92	d1jr1a4	Alignment	not modelled	97.9	15	Fold: CBS-domain pair Superfamily: CBS-domain pair Family: CBS-domain pair
93	d2a29a1	Alignment	not modelled	75.0	14	Fold: Metal cation-transporting ATPase, ATP-binding domain N Superfamily: Metal cation-transporting ATPase, ATP-binding domain N Family: Metal cation-transporting ATPase, ATP-binding domain N
94	c2arfA_	Alignment	not modelled	59.8	16	PDB header: hydrolase Chain: A: PDB Molecule: wilson disease atpase; PDBTitle: solution structure of the wilson atpase n-domain in the2 presence of atp
95	c4onxB_	Alignment	not modelled	46.1	29	PDB header: transferase Chain: B: PDB Molecule: sensor histidine kinase; PDBTitle: 2.8 angstrom crystal structure of sensor domain of histidine kinase2 from clostridium perfringens.
96	c2koyA_	Alignment	not modelled	37.0	16	PDB header: metal transport Chain: A: PDB Molecule: copper-transporting atpase 2; PDBTitle: structure of the e1064a mutant of the n-domain of wilson disease2 associated protein
97	d1lcyA2	Alignment	not modelled	31.6	23	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
98	c2rcel_	Alignment	not modelled	30.9	38	PDB header: hydrolase Chain: I: PDB Molecule: protease degs; PDBTitle: dfp modified degs delta pdz
99	c3nziA_	Alignment	not modelled	29.7	31	PDB header: hydrolase/hydrolase substrate Chain: A: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
100	d1diva1	Alignment	not modelled	27.6	33	Fold: Ribosomal protein L9 C-domain Superfamily: Ribosomal protein L9 C-domain Family: Ribosomal protein L9 C-domain
101	c3nwuB_	Alignment	not modelled	27.5	31	PDB header: hydrolase Chain: B: PDB Molecule: serine protease htra1; PDBTitle: substrate induced remodeling of the active site regulates htra12 activity
102	d1ky9a2	Alignment	not modelled	26.1	31	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
103	c3k2tA_	Alignment	not modelled	25.8	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo2511 protein; PDBTitle: crystal structure of lmo2511 protein from listeria2

						monocytogenes, northeast structural genomics consortium3 target lkr84a
104	c3k6zA_	Alignment	not modelled	25.6	31	PDB header: hydrolase Chain: A: PDB Molecule: possible membrane-associated serine protease; PDBTitle: crystal structure of rv3671c protease, inactive form
105	c3stiC_	Alignment	not modelled	24.6	31	PDB header: hydrolase Chain: C: PDB Molecule: protease degq; PDBTitle: crystal structure of the protease domain of degq from escherichia coli
106	d2gycf1	Alignment	not modelled	23.6	29	Fold: Ribosomal protein L9 C-domain Superfamily: Ribosomal protein L9 C-domain Family: Ribosomal protein L9 C-domain
107	c6o6dA_	Alignment	not modelled	23.2	10	PDB header: ligase Chain: A: PDB Molecule: translation initiation factor if-3; PDBTitle: n-terminal domain of translation initiation factor if-3 from2 helicobacter pylori
108	d2qf3a1	Alignment	not modelled	21.0	38	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Prokaryotic proteases
109	c5y28B_	Alignment	not modelled	20.9	54	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic serine endoprotease degp-like; PDBTitle: crystal structure of h. pylori htra with pdz2 deletion
110	c3ka5A_	Alignment	not modelled	20.6	9	PDB header: chaperone Chain: A: PDB Molecule: ribosome-associated protein y (psrp-1); PDBTitle: crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a